

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Sep 27 13:54:46 EDT 2007

=====

Application No: 10789355 Version No: 2.0

Input Set:

Output Set:

Started: 2007-09-21 08:46:54.036
Finished: 2007-09-21 08:46:58.740
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 704 ms
Total Warnings: 30
Total Errors: 0
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2007-09-21 08:46:54.036
Finished: 2007-09-21 08:46:58.740
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 704 ms
Total Warnings: 30
Total Errors: 0
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> BOEHRINGER INGELHEIM (CANADA) LTD.

<120> SELF REPLICATING RNA MOLECULE FROM
HEPATITIS C VIRUS

<130> 13/083-3-D2

<140> 10789355

<141> 2004-02-27

<150> 60/257,857

<151> 2000-12-22

<150> 10/029,907

<151> 2001-12-21

<160> 30

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 8639

<212> DNA

<213> HCV

<220>

<221> CDS

<222> (1803)....(8408)

<400> 1

ggccagcccc cgattgggg cgacactcca ccatagatca ctccttgcg aggaactact 60
gtcttcacgc agaaagcgta tagccatggc gtttagtatga gtgtcggtca gcctccagga 120
ccccccctcc cgggagagcc atagttgtct gcgaaaccgg ttagtacacc ggaattgcca 180
ggacgaccgg gtcttttttggatcaaccc gctcaatgcc tggagatttg ggcgtgcccc 240
cgcgagactg ctagccgagt agtgttgggt cgcgaaaggc cttgtggta tgcctgatag 300
ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca ccatgagcac gaatcctaaa 360
cctcaaagaa aaaccaaagg ggcgcctatg attgaacaag atggattgca cgcaggatct 420
ccggccgctt ggggtggagag gctattcggc tatgactggg cacaacagac aatcggctgc 480
tctgatgccc ccgtgttccc gctgtcagcg cagggggccc cggttttttt tggcaagacc 540
gacctgtccc gtgcctgaa tgaactgcg gacgaggcag cgcggctatc gtggctggcc 600
acgacggggcg ttccctgcgc agctgtgtc gacgttgtca ctgaagcggg aaggggactgg 660
ctgctattgg gcgaagtgcg gggggcaggat ctccctgtcat ctcaccttgc tcctgcccag 720
aaagtatcca tcatggctga tgcaatgcgg cggctgcata cgcttgcattt ggctacatgc 780
ccattcgacc accaagcgaa acatcgcatc gagcgagcac gtactcgat ggaagccgg 840
cttgcgatc aggatgatct ggacgaaagag catcaggggc tcgcgcagc cgaactgttc 900
gccaggctca aggcgcgcat gcccgcacggc gaggatctcg tctgtacccca tggcgatgcc 960
tgcttgcga atatcatgtt gggaaatggc cgctttctg gattcatcga ctgtggccgg 1020
ctgggtgtgg cggaccgcta tcaggacata gcggtggcta cccgtgatat tgctgaagag 1080
cttggcggcg aatgggctga cgcgttccct gtgttttacg gtatcgccgc tcccgattcg 1140
cagcgcatcg ctttctatcg ctttcttgc gatgttttctt gatgtcgccgc ccagatgtta 1200
acagaccaca acgggttccc tctagcggga tcaattccgc cccccccctt aacgttactg 1260
gccgaagccg ctggaaataa ggccgggtgtg cggttgcata tatgttattt tccaccat 1320
tgccgttccctt tggcaatgtg agggcccgga aacctggccc tggcttcttgc acgagcatc 1380

ctaggggtct ttcccctctc gccaaaggaa tgcaaggtct gttgaatgtc gtgaaggaag 1440
 cagttcctct ggaagcttct tgaagacaaa caacgtctgt agcgaccctt tgcaggcagc 1500
 ggaacccccc acctggcgac aggtgcctct gcggccaaaa gccacgtgta taagatacac 1560
 ctgcaaaggc ggcacaaccc cagtgcacac ttgtgagttg gatagttgtg gaaagagtca 1620
 aatggctctc ctcaagcgta ttcaacaagg ggctgaagga tgcccagaag gtacccatt 1680
 gtatggatc tgatctgggg cctcggtgca catgcttac atgtgtttag tcgaggttaa 1740
 aaaacgtcta ggccccccga accacgggga cgtggtttc ctttggaaaaa cacgataata 1800
 cc atg gac cgg gag atg gca gca tcg tgc gga ggc gcg gtt ttc gta 1847
 Met Asp Arg Glu Met Ala Ala Ser Cys Gly Gly Ala Val Phe Val
 1 5 10 15

ggt ctg ata ctc ttg acc ttg tca ccg cac tat aag ctg ttc ctc gct 1895
 Gly Leu Ile Leu Leu Thr Leu Ser Pro His Tyr Lys Leu Phe Leu Ala
 20 25 30

agg ctc ata tgg tgg tta caa tat ttt atc acc agg gcc gag gca cac 1943
 Arg Leu Ile Trp Trp Leu Gln Tyr Phe Ile Thr Arg Ala Glu Ala His
 35 40 45

ttg caa gtg tgg atc ccc ccc ctc aac gtt cgg ggg ggc cgc gat gcc 1991
 Leu Gln Val Trp Ile Pro Pro Leu Asn Val Arg Gly Gly Arg Asp Ala
 50 55 60

gtc atc ctc ctc acg tgc gcg atc cac cca gag cta atc ttt acc atc 2039
 Val Ile Leu Leu Thr Cys Ala Ile His Pro Glu Leu Ile Phe Thr Ile
 65 70 75

acc aaa atc ttg ctc gcc ata ctc ggt cca ctc atg gtg ctc cag gct 2087
 Thr Lys Ile Leu Leu Ala Ile Leu Gly Pro Leu Met Val Leu Gln Ala
 80 85 90 95

ggt ata acc aaa gtg ccg tac ttc gtg cgc gca cac ggg ctc att cgt 2135
 Gly Ile Thr Lys Val Pro Tyr Phe Val Arg Ala His Gly Leu Ile Arg
 100 105 110

gca tgc atg ctg gtg cgg aag gtt gct ggg ggt cat tat gtc caa atg 2183
 Ala Cys Met Leu Val Arg Lys Val Ala Gly Gly His Tyr Val Gln Met
 115 120 125

gct ctc atg aag ttg gcc gca ctg aca ggt acg tac gtt tat gac cat 2231
 Ala Leu Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp His
 130 135 140

ctc acc cca ctg cgg gac tgg gcc cac gcg ggc cta cga gac ctt gcg 2279
 Leu Thr Pro Leu Arg Asp Trp Ala His Ala Gly Leu Arg Asp Leu Ala
 145 150 155

gtg gca gtt gag ccc gtc gtc ttc tct gat atg gag acc aag gtt atc 2327
 Val Ala Val Glu Pro Val Val Phe Ser Asp Met Glu Thr Lys Val Ile
 160 165 170 175

acc tgg ggg gca gac acc gcg gcg tgt ggg gac atc atc ttg ggc ctg 2375
 Thr Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Leu Gly Leu
 180 185 190

ccc gtc tcc gcc cgc agg ggg agg gag ata cat ctg gga ccg gca gac 2423
 Pro Val Ser Ala Arg Arg Gly Arg Glu Ile His Leu Gly Pro Ala Asp

195	200	205	
agc ctt gaa ggg cag ggg tgg cga ctc ctc gcg cct att acg gcc tac			2471
Ser Leu Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala Tyr			
210	215	220	
tcc caa cag acg cga ggc cta ctt ggc tgc atc atc act acg ctc aca			2519
Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr			
225	230	235	
ggc cg ^g gac agg aac cag gtc gag ggg gag gtc caa gtg gtc tcc acc			2567
Gly Arg Asp Arg Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr			
240	245	250	255
gca aca caa tct ttc ctg gcg acc tgc gtc aat ggc gtg tgt tgg act			2615
Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr			
260	265	270	
gtc tat cat ggt gcc ggc tca aag acc ctt gcc ggc cca aag ggc cca			2663
Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro			
275	280	285	
atc acc caa atg tac acc aat gtg gac cag gac ctc gtc ggc tgg caa			2711
Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln			
290	295	300	
g ^c g ccc ccc ggg g ^c g cgt tcc ttg aca cca tgc acc tgc ggc agc tcg			2759
Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser			
305	310	315	
gac ctt tac ttg gtc acg agg cat gcc gat gtc att ccg gtg cgc cgg			2807
Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg			
320	325	330	335
cg ^g ggc gac agc agg ggg agc cta ctc tcc ccc agg ccc gtc tcc tac			2855
Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr			
340	345	350	
ttg aag ggc tct tcg ggc ggt cca ctg ctc tgc ccc tcg ggg cac gct			2903
Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala			
355	360	365	
gtg ggc atc ttt cgg gct gcc gtg tgc acc cga ggg gtt g ^c g aag g ^c g			2951
Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala			
370	375	380	
gtg gac ttt gta ccc gtc gag tct atg gaa acc act atg cgg tcc ccg			2999
Val Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro			
385	390	395	
gtc ttc acg gac aac tcg tcc cct ccg gcc gta ccg cag aca ttc cag			3047
Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro Gln Thr Phe Gln			
400	405	410	415
gtg gcc cat cta cac gcc cct act ggt agc ggc aag agc act aag gtg			3095
Val Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val			
420	425	430	

ccg gct gcg tat gca gcc caa ggg tat aag gtg ctt gtc ctg aac ccg	3143		
Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro			
435	440	445	
tcc gtc gcc gcc acc cta ggt ttc ggg gcg tat atg tct aag gca cat	3191		
Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His			
450	455	460	
ggt atc gac cct aac atc aga acc ggg gta agg acc atc acc acg ggt	3239		
Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly			
465	470	475	
gcc ccc atc acg tac tcc acc tat ggc aag ttt ctt gcc gac ggt ggt	3287		
Ala Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly			
480	485	490	495
tgc tct ggg ggc gcc tat gac atc ata ata tgt gat gag tgc cac tca	3335		
Cys Ser Gly Gly Ala Tyr Asp Ile Ile Cys Asp Glu Cys His Ser			
500	505	510	
act gac tcg acc act atc ctg ggc atc ggc aca gtc ctg gac caa gcg	3383		
Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala			
515	520	525	
gag acg gct gga gcg cga ctc gtc gtg ctc gcc acc gct acg cct ccg	3431		
Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro			
530	535	540	
gga tcg gtc acc gtg cca cat cca aac atc gag gag gtg gct ctg tcc	3479		
Gly Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser			
545	550	555	
agc act gga gaa atc ccc ttt tat ggc aaa gcc atc ccc atc gag acc	3527		
Ser Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Thr			
560	565	570	575
atc aag ggg ggg agg cac ctc att ttc tgc cat tcc aag aag aaa tgt	3575		
Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys			
580	585	590	
gat gag ctc gcc gcg aag ctg tcc ggc ctc gga ctc aat gct gta gca	3623		
Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Leu Asn Ala Val Ala			
595	600	605	
tat tac cgg ggc ctt gat gta tcc gtc ata cca act agc gga gac gtc	3671		
Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val			
610	615	620	
att gtc gta gca acg gac gct cta atg acg ggc ttt acc ggc gat ttc	3719		
Ile Val Val Ala Thr Asp Ala Leu Met Thr Gly Phe Thr Gly Asp Phe			
625	630	635	
gac tca gtg atc gac tgc aat aca tgt gtc acc cag aca gtc gac ttc	3767		
Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe			
640	645	650	655

agc ctg gac ccg acc ttc acc att gag acg acg acc gtg cca caa gac Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp	660	665	670	3815	
gcg gtg tca cgc tcg cag cgg cga ggc agg act ggt agg ggc agg atg Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Met	675	680	685	3863	
ggc att tac agg ttt gtg act cca gga gaa cgg ccc tcg ggc atg ttc Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe	690	695	700	3911	
gat tcc tcg gtt ctg tgc gag tgc tat gac gcg ggc tgt gct tgg tac Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr	705	710	715	3959	
gag ctc acg ccc gcc gag acc tca gtt agg ttg cgg gct tac cta aac Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn	720	725	730	735	4007
aca cca ggg ttg ccc gtc tgc cag gac cat ctg gag ttc tgg gag agc Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser	740	745	750	4055	
gtc ttt aca ggc ctc acc cac ata gac gcc cat ttc ttg tcc cag act Val Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr	755	760	765	4103	
aag cag gca gga gac aac ttc ccc tac ctg gta gca tac cag gct acg Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr	770	775	780	4151	
gtg tgc gcc agg gct cag gct cca cct cca tcg tgg gac caa atg tgg Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp	785	790	795	4199	
aag tgt ctc ata cgg cta aag cct acg ctg cac ggg cca acg ccc ctg Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu	800	805	810	815	4247
ctg tat agg ctg gga gcc gtt caa aac gag gtt act acc aca cac ccc Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Thr His Pro	820	825	830	4295	
ata acc aaa tac atc atg gca tgc atg tcg gct gac ctg gag gtc gtc Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val	835	840	845	4343	
acg agc acc tgg gtg ctg gta ggc gga gtc cta gca gct ctg gcc gcg Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala	850	855	860	4391	
tat tgc ctg aca aca ggc agc gtg gtc att gtg ggc agg atc atc ttg Tyr Cys Leu Thr Thr Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	865	870	875	4439	
tcc gga aag ccg gcc atc att ccc gac agg gaa gtc ctt tac cgg gag				4487	

Ser	Gly	Lys	Pro	Ala	Ile	Ile	Pro	Asp	Arg	Glu	Val	Leu	Tyr	Arg	Glu		
880				885				890			895						
ttc	gat	atg	gaa	gag	tgc	gcc	tca	cac	ctc	cct	tac	atc	gaa	cag		4535	
Phe	Asp	Glu	Met	Glu	Glu	Cys	Ala	Ser	His	Leu	Pro	Tyr	Ile	Glu	Gln		
			900				905						910				
gga	atg	cag	ctc	gcc	gaa	caa	ttc	aaa	cag	aag	gca	atc	ggg	ttg	ctg		4583
Gly	Met	Gln	Leu	Ala	Glu	Gln	Phe	Lys	Gln	Lys	Ala	Ile	Gly	Leu	Leu		
			915				920					925					
caa	aca	gcc	acc	aag	caa	gcg	gag	gct	gct	ccc	gtg	gtg	gaa	tcc		4631	
Gln	Thr	Ala	Thr	Lys	Gln	Ala	Glu	Ala	Ala	Ala	Pro	Val	Val	Glu	Ser		
			930				935					940					
aag	tgg	cgg	acc	ctc	gaa	gcc	ttc	tgg	gcg	aag	cat	atg	tgg	aat	ttc		4679
Lys	Trp	Arg	Thr	Leu	Glu	Ala	Phe	Trp	Ala	Lys	His	Met	Trp	Asn	Phe		
			945				950					955					
atc	agc	ggg	ata	caa	tat	tta	gca	ggc	ttg	tcc	act	ctg	cct	ggc	aac		4727
Ile	Ser	Gly	Ile	Gln	Tyr	Leu	Ala	Gly	Leu	Ser	Thr	Leu	Pro	Gly	Asn		
			960				965					970		975			
ccc	gcg	ata	gca	tca	ctg	atg	gca	ttc	aca	gcc	tct	atc	acc	agc	ccg		4775
Pro	Ala	Ile	Ala	Ser	Leu	Met	Ala	Phe	Thr	Ala	Ser	Ile	Thr	Ser	Pro		
			980				985					990					
ctc	acc	acc	caa	cat	acc	ctc	ctg	ttt	aac	atc	ctg	ggg	gga	tgg	gtg		4823
Leu	Thr	Thr	Gln	His	Thr	Leu	Leu	Phe	Asn	Ile	Leu	Gly	Gly	Trp	Val		
			995				1000					1005					
gcc	gcc	caa	ctt	gct	ccc	agc	gct	gct	tct	gct	ttc	gta	ggc	gcc		4871	
Ala	Ala	Gln	Leu	Ala	Pro	Pro	Ser	Ala	Ala	Ser	Ala	Phe	Val	Gly	Ala		
			1010				1015					1020					
ggc	atc	gct	gga	gcg	gct	gtt	ggc	agc	ata	ggc	ctt	ggg	aag	gtg	ctt		4919
Gly	Ile	Ala	Gly	Ala	Ala	Val	Gly	Ser	Ile	Gly	Leu	Gly	Lys	Val	Leu		
			1025				1030					1035					
gtg	gat	att	ttg	gca	ggt	tat	gga	gca	ggg	gtg	gca	ggc	gct	ctc	gtg		4967
Val	Asp	Ile	Leu	Ala	Gly	Tyr	Gly	Ala	Gly	Val	Ala	Gly	Ala	Leu	Val		
			1040				1045					1050		1055			
gcc	ttt	aag	gtc	atg	agc	ggc	gag	atg	ccc	tcc	acc	gag	gac	ctg	gtt		5015
Ala	Phe	Lys	Val	Met	Ser	Gly	Glu	Met	Pro	Ser	Thr	Glu	Asp	Leu	Val		
			1060				1065					1070					
aac	cta	ctc	cct	gct	atc	ctc	tcc	cct	ggc	gcc	cta	gtc	gtc	ggg	gtc		5063
Asn	Leu	Leu	Pro	Ala	Ile	Leu	Ser	Pro	Gly	Ala	Leu	Val	Val	Gly	Val		
			1075				1080					1085					
gtg	tgc	gca	gcg	ata	ctg	cgt	cgg	cac	gtg	ggc	cca	ggg	gag	ggg	gct		5111
Val	Cys	Ala	Ala	Ile	Leu	Arg	Arg	His	Val	Gly	Pro	Gly	Glu	Gly	Ala		
			1090				1095					1100					
gtg	cag	tgg	atg	aac	cg	ctg	ata	g	t	tc	g	cg	gg	gt	aa		5159
Val	Gln	Trp	Met	Asn	Arg	Leu	Ile	Ala	Phe	Ala	Ser	Arg	Gly	Asn	His		

1105	1110	1115	
gtc tcc ccc acg cac tat gtg cct gag agc gac gct gca gca cgt gtc			5207
Val Ser Pro Thr His Tyr Val Pro Glu Ser Asp Ala Ala Ala Arg Val			
1120	1125	1130	1135
act cag atc ctc tct agt ctt acc atc act cag ctg ctg aag agg ctt			5255
Thr Gln Ile Leu Ser Ser Leu Thr Ile Thr Gln Leu Leu Lys Arg Leu			
1140	1145	1150	
cac cag tgg atc aac gag gac tgc tcc acg cca tgc tcc ggc tcg tgg			5303
His Gln Trp Ile Asn Glu Asp Cys Ser Thr Pro Cys Ser Gly Ser Trp			
1155	1160	1165	
cta aga gat gtt tgg gat tgg ata tgc acg gtg ttg act gat ttc aag			5351
Leu Arg Asp Val Trp Asp Trp Ile Cys Thr Val Leu Thr Asp Phe Lys			
1170	1175	1180	
acc tgg ctc cag tcc aag ctc ctg ccg cga ttg ccg gga gtc ccc ttc			5399
Thr Trp Leu Gln Ser Lys Leu Leu Pro Arg Leu Pro Gly Val Pro Phe			
1185	1190	1195	
ttc tca tgt caa cgt ggg tac aag gga gtc tgg cgg ggc gac ggc atc			5447
Phe Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg Gly Asp Gly Ile			
1200	1205	1210	1215
atg caa acc acc tgc cca tgt gga gca cag atc acc gga cat gtg aaa			5495
Met Gln Thr Thr Cys Pro Cys Gly Ala Gln Ile Thr Gly His Val Lys			
1220			